

## SEQUENCE LISTING

<110> Pharmacia & Upjohn  
Gu, Yizhong

<120> Canine L-PBE Sequences

<130> 1492

<150> 60/437,530  
<151> 2002-12-31

<160> 16

<170> PatentIn version 3.1

<210> 1  
<211> 2169  
<212> DNA  
<213> Canis familiaris

<400> 1	
atggccgagt atacgcggct gcacaacgcc ttggcggtga tccgcctccg aaacccgccc	60
gtcaacgcca tcagtgacggc tgtactccgt ggaataaaag acggatttgc gaaagctacc	120
acagaccgta cagtaaaaagg tattgtgctt tgccggagcag atggcaaatt ctctgcaggt	180
gctgatatcc acagctttgg tgagccccaga aagtctgact ttgtacttagg acatata>tagta	240
gatgaaatac agagaactga gaagccccgtg gtggcagcta ttcaaggcct ggcttttagga	300
gggggactgg agctggcgct gggctgtcac tataggattt ctcattgcaga ggctcaaatt	360
ggcttcccag aagtccacaactt aggaatccctt cctgggtgcaaa gaggaacccca gettctcccc	420
agactcattt gaggttcctgc tgcacttgac ttaatttacct caggaagaca tgttttggca	480
gatgaagcac tcaagctggg tatccttagat gaaattgtga actccagaccc ggttgaagaa	540
gcaatcaaata tagccccagag aatctctgtat caatctcttag aatccccgttag actctgcac	600
aagccaaatttcc agagcttgcc caacatggag agtattttca gtgaagccct ttcgaagatg	660
cagaaggcage atccccgggtg ctttgcgttca gagacttggc tccgtgcagt ccaggctgccc	720
gtgcatttgc ctttgcgttca gagacttggc tccgtgcagt ccaggctgccc	780
aaatcaggcaggc aggcttagagc ctttgcgttca gagacttggc tccgtgcagt ccaggctgccc	840
tggtcaactc ctttgcgttca gagacttggc tccgtgcagt ccaggctgccc	900
ggcggttgcgttca gagacttggc tccgtgcagt ccaggctgccc	960
atcccaatccatc ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1020
actaccctctt ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1080
ccaaaacccca gtttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1140
gcgttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1200
aagccaaatttcc ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1260
tccactgtatc ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1320
aatttatcaa aaaatggaa aaaaatttggaa gtttttttttgcgttca gagacttggc tccgtgcagt	1380
ggcaatcgaa ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1440
aggccaggagg agatagatca gtttttttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1500
gtgtcagatc ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1560
ggacccatgg ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1620
atccctgtatc ttttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1680
caatatgata agccatttggg taggatttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1740
aaacccatggg taggatttgcgttca gagacttggc tccgtgcagt ccaggctgccc	1800



Val His Cys Pro Tyr Glu Val Gly Ile Gln Lys Glu Lys Glu Leu Phe  
 245 250 255  
  
 Met Tyr Leu Gln Lys Ser Gly Gln Ala Arg Ala Leu Gln Tyr Ala Phe  
 260 265 270  
  
 Phe Ala Glu Arg Asn Ala Thr Lys Trp Ser Thr Pro Ser Gly Ala Ser  
 275 280 285  
  
 Trp Lys Thr Ala Ile Ala Gln Pro Ile Ser Ser Val Gly Val Val Gly  
 290 295 300  
  
 Leu Gly Thr Met Gly Arg Gly Ile Val Val Ser Leu Ala Lys Ala Lys  
 305 310 315 320  
  
 Ile Pro Val Ile Ala Val Glu Ser Asp Lys Lys Gln Leu Glu Thr Ala  
 325 330 335  
  
 Asp Met Ile Ile Thr Thr Leu Leu Glu Lys Glu Ala Ser Lys Met Gln  
 340 345 350  
  
 Arg Ser Ser His Pro Ser Leu Gly Pro Lys Pro Arg Leu Thr Thr Ser  
 355 360 365  
  
 Met Lys Glu Leu Gly Val Asp Leu Val Ile Glu Ala Val Phe Glu  
 370 375 380  
  
 Glu Ile Asn Leu Lys Lys Arg Val Phe Ala Glu Leu Ser Ala Ile Cys  
 385 390 395 400  
  
 Lys Pro Glu Ala Phe Leu Cys Thr Asn Thr Ser Ala Leu Asp Ile Asp  
 405 410 415  
  
 Glu Ile Ala Ser Ser Thr Asp Arg Pro His Leu Val Ile Gly Thr His  
 420 425 430  
  
 Phe Phe Ser Pro Ala His Val Met Lys Leu Leu Glu Ile Ile Pro Ser  
 435 440 445  
  
 Gln Tyr Ser Ser Pro Thr Thr Ile Ala Thr Val Met Asn Leu Ser Lys  
 450 455 460  
  
 Lys Ile Lys Lys Ile Gly Val Val Gly Asn Cys Phe Gly Phe Val  
 465 470 475 480  
  
 Gly Asn Arg Met Leu Lys Pro Tyr Tyr Asn Gln Thr Tyr Phe Leu Leu  
 485 490 495  
  
 Glu Glu Gly Ser Arg Pro Glu Glu Ile Asp Gln Val Leu Glu Glu Phe  
 500 505 510  
  
 Gly Phe Lys Met Gly Pro Phe Arg Val Ser Asp Leu Ala Gly Leu Asp  
 515 520 525  
  
 Val Gly Trp Lys Ser Arg Gln Gly Gln Gly Leu Thr Gly Pro Met Val  
 530 535 540  
  
 Pro Ser Gly Thr Pro Ala Arg Lys Arg Gly Asn Arg Arg Tyr Cys Pro  
 545 550 555 560

Ile Pro Asp Leu Leu Cys Glu Ser Gly Arg Phe Gly Gln Lys Thr Gly  
565 570 575

Lys Gly Trp Tyr Gln Tyr Asp Lys Pro Leu Gly Arg Ile His Lys Pro  
580 585 590

Asp Pro Trp Leu Ser Glu Phe Leu Ser Gln Tyr Arg Lys Thr Tyr His  
595 600 605

Ile Glu Pro Arg Ile Ile Ser Gln Asp Glu Ile Leu Glu Arg Cys Leu  
610 615 620

Tyr Ser Leu Ile Asn Glu Ala Phe Arg Ile Leu Gly Glu Gly Met Ala  
625 630 635 640

Ala Asp Pro Glu His Ile Asp Val Val Tyr Leu His Gly Tyr Gly Trp  
645 650 655

Pro Arg His Arg Gly Gly Pro Met Phe Tyr Ala Ser Thr Val Gly Leu  
660 665 670

Pro Thr Val Leu Glu Lys Leu Gln Lys Tyr Tyr Arg Gln Asn Pro Asp  
675 680 685

Ile Pro Gln Leu Glu Pro Cys Asp Tyr Leu Lys Lys Leu Ala Ser Leu  
690 695 700

Gly Asn Pro Pro Leu Lys Glu Trp Gln Ser Leu Ala Gly Ser Pro Ser  
705 710 715 720

Ser Lys Leu

<210> 3  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Primer Sequence

<400> 3  
atggccgagt atacgcggct gcacaacgcc

30

<210> 4  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<223> Primer Sequence

<400> 4  
tcacaattta ctgcttagggg agcctgccaa g

31

<210> 5  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Primer Sequence

<400> 5  
cttatattca cttatcaatg aagc

24

<210> 6		
<211> 23		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer Sequence		
<400> 6		
gtagttgttag gtaactgttt tgg		23
<210> 7		
<211> 24		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer Sequence		
<400> 7		
gacactctaa aaggcccattt ttttg		24
<210> 8		
<211> 22		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer Sequence		
<400> 8		
cctcaaatac tgcttcaatg ac		22
<210> 9		
<211> 23		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer Sequence		
<400> 9		
gattgcttct tcaaccgggt ctg		23
<210> 10		
<211> 22		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer Sequence		
<400> 10		
cacttgactt aattacctca gg		22
<210> 11		
<211> 2169		
<212> DNA		
<213> Homo sapiens		
<400> 11		
atggccgagt atacgcggct gcacaacgcc ttggcgctaa tccgcctccg aaacccggcg		60
gtcaacgcga tcagtcgac tttactccgt gatataaaag aaggactaca gaaagctgga		120
agagaccata caataaaaagc cattgtgatt tgtggagcag agggcaaatt ttctgcaggt		180
gctgatatttc gtggcttcag tgctcctagg acatttggcc ttatactggg acatgttagta		240
gatgaaatac agagaaaatga gaagccccgtg gtggcagcaa tccaaggcat ggctttcgga		300
gggggactag agctggccct gggctgtcac tataggattt cccacgcaga cgctcaagtt		360
ggcttaccag aagttacact tggacttctc cctggtgcaa gaggaaccca gtttctcccc		420
agactcactg gagttcctgc tgcacttgac ttaattacct caggaagacg tatttttagca		480

gatgaagcac tcaagctggg cattctagat aaagttgtaa actcagaccc gggttaagaa	540
gcaatcagat ttgcctcagag agtttcagat caacctctag aatcccgtag actctgcaac	600
aagccaattc agagcttgcc caacatggac agcatttta gtgaggccct cttgaagatg	660
cggaggcagc accctgggtg tcttcacag gaggcttgc tccgtgcagt ccaggctgct	720
gtcagttatc cctatgaagt gggcatcaag aaggaggagg agctgtttct atatcttttg	780
caatcaggc aggcttagagc cctgcaatat gctttttcg ctgaaaggaa agcaaataag	840
tggtcaactc cctccggc acatcgaaa acagcatcg cgccgcctgt ctccctcgtt	900
ggtgttggc gcttggaaac aatggccoga ggcattgtca tttttttgc aaggccagg	960
atccctgtga ttggttaga ctggacaaa aaccagctag caactgcaaa caagatgata	1020
acccctgtct tggaaaaaga agcctccaaa atgcaacaga gcggccaccc ttggcagga	1080
ccaaaaccca gtttaacttc atctgtgaag gagcttggc gtgttagatt agtcattgaa	1140
gcagtatttgc agggaaatgag cctgaagaag caggttttgc tgaactctc agctgtgtgc	1200
aaaccagaag cattttgtg cactaatact tcagccctgg atgttgcattttgc gattgcttct	1260
tccactgatc gtcctcaattt ggtcattggc acccacttct tttcgccagc tcattgtcatg	1320
aagggtttag aggttattcc cagccaatac tcttccccca ctaccattgc cactgttatg	1380
aacttatcaa aaaagattaa aaagatttggc gtcgtgttag gcaactgttt tggatttgc	1440
ggaaatcgaa tggtaatcc ttactacaat caggcatatt tcttggtaga agaaggcagc	1500
aaaccagagg aggttagatca ggtgctggaa gagtttggc ttaaaatggg accttttgc	1560
gtgtctgatc ttgtgggtt ggatgtggc tggaaatcta gaaaggggca aggtcttact	1620
ggacctacat tgctccagg aactccctgcc cggaaaaagg gtaataggag gtactgccc	1680
atccctgtat tgctctgtat attaggacgc tttggccaga agacaggtaa ggggttgc	1740
caatatgaca agccatttggg taggattcac aaacctgtat cctggcttc cacattcc	1800
tcacggatata gaaaacccca tcacatttgc ccacgtacca ttagccagg ttagatcctt	1860
gaacgctgat tatattact tatcaatgc gcattccgtat tcttgggaga agggatagct	1920
gctagcccag agcacattgc tggatgttat ttagatggat atggatgcgc aaggcacaag	1980
ggccggccca tggatgttatgc ttccacagtt ggggttgc cagttctaga gaaattgcag	2040
aaatattaca ggcagaaccc tgatattccc caactggcgc caagtgcata tctaaaaaaa	2100
ctggcttctc agggaaaccc tccctgaaa gaatggcaaa gcttggcagg ctccctagc	2160
agtaaaattg	2169

<210> 12  
 <211> 723  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met Ala Glu Tyr Thr Arg Leu His Asn Ala Leu Ala Leu Ile Arg Leu  
 1 5 10 15

Arg Asn Pro Pro Val Asn Ala Ile Ser Thr Thr Leu Leu Arg Asp Ile  
 20 25 30

Lys Glu Gly Leu Gln Lys Ala Gly Arg Asp His Thr Ile Lys Ala Ile  
 35 40 45

Val Ile Cys Gly Ala Glu Gly Lys Phe Ser Ala Gly Ala Asp Ile Arg  
 50 55 60

Gly Phe Ser Ala Pro Arg Thr Phe Gly Leu Ile Leu Gly His Val Val  
 65 70 75 80

Asp Glu Ile Gln Arg Asn Glu Lys Pro Val Val Ala Ala Ile Gln Gly  
 85 90 95

Met Ala Phe Gly Gly Leu Glu Leu Ala Leu Gly Cys His Tyr Arg  
 100 105 110

Ile Ala His Ala Asp Ala Gln Val Gly Leu Pro Glu Val Thr Leu Gly  
 115 120 125

Leu Leu Pro Gly Ala Arg Gly Thr Gln Leu Leu Pro Arg Leu Thr Gly  
 130 135 140

Val Pro Ala Ala Leu Asp Leu Ile Thr Ser Gly Arg Arg Ile Leu Ala  
 145 150 155 160

Asp Glu Ala Leu Lys Leu Gly Ile Leu Asp Lys Val Val Asn Ser Asp  
 165 170 175

Pro Val Glu Glu Ala Ile Arg Phe Ala Gln Arg Val Ser Asp Gln Pro  
 180 185 190

Leu Glu Ser Arg Arg Leu Cys Asn Lys Pro Ile Gln Ser Leu Pro Asn  
 195 200 205

Met Asp Ser Ile Phe Ser Glu Ala Leu Leu Lys Met Arg Arg Gln His  
 210 215 220

Pro Gly Cys Leu Ala Gln Glu Ala Cys Val Arg Ala Val Gln Ala Ala  
 225 230 235 240

Val Gln Tyr Pro Tyr Glu Val Gly Ile Lys Lys Glu Glu Glu Leu Phe  
 245 250 255

Leu Tyr Leu Leu Gln Ser Gly Gln Ala Arg Ala Leu Gln Tyr Ala Phe  
 260 265 270

Phe Ala Glu Arg Lys Ala Asn Lys Trp Ser Thr Pro Ser Gly Ala Ser  
 275 280 285

Trp Lys Thr Ala Ser Ala Arg Pro Val Ser Ser Val Gly Val Val Gly  
 290 295 300

Leu Gly Thr Met Gly Arg Gly Ile Val Ile Ser Phe Ala Arg Ala Arg  
 305 310 315 320

Ile Pro Val Ile Gly Val Asp Ser Asp Lys Asn Gln Leu Ala Thr Ala  
 325 330 335

Asn Lys Met Ile Thr Ser Val Leu Glu Lys Glu Ala Ser Lys Met Gln  
 340 345 350

Gln Ser Gly His Pro Trp Ser Gly Pro Lys Pro Arg Leu Thr Ser Ser  
 355 360 365

Val Lys Glu Leu Gly Gly Val Asp Leu Val Ile Glu Ala Val Phe Glu  
 370 375 380

Glu Met Ser Leu Lys Lys Gln Val Phe Ala Glu Leu Ser Ala Val Cys  
 385                   390                   395                   400  
  
 Lys Pro Glu Ala Phe Leu Cys Thr Asn Thr Ser Ala Leu Asp Val Asp  
 405                   410                   415  
  
 Glu Ile Ala Ser Ser Thr Asp Arg Pro His Leu Val Ile Gly Thr His  
 420                   425                   430  
  
 Phe Phe Ser Pro Ala His Val Met Lys Leu Leu Glu Val Ile Pro Ser  
 435                   440                   445  
  
 Gln Tyr Ser Ser Pro Thr Thr Ile Ala Thr Val Met Asn Leu Ser Lys  
 450                   455                   460  
  
 Lys Ile Lys Lys Ile Gly Val Val Val Gly Asn Cys Phe Gly Phe Val  
 465                   470                   475                   480  
  
 Gly Asn Arg Met Leu Asn Pro Tyr Tyr Asn Gln Ala Tyr Phe Leu Leu  
 485                   490                   495  
  
 Glu Glu Gly Ser Lys Pro Glu Glu Val Asp Gln Val Leu Glu Glu Phe  
 500                   505                   510  
  
 Gly Phe Lys Met Gly Pro Phe Arg Val Ser Asp Leu Ala Gly Leu Asp  
 515                   520                   525  
  
 Val Gly Trp Lys Ser Arg Lys Gly Gln Gly Leu Thr Gly Pro Thr Leu  
 530                   535                   540  
  
 Leu Pro Gly Thr Pro Ala Arg Lys Arg Gly Asn Arg Arg Tyr Cys Pro  
 545                   550                   555                   560  
  
 Ile Pro Asp Val Leu Cys Glu Leu Gly Arg Phe Gly Gln Lys Thr Gly  
 565                   570                   575  
  
 Lys Gly Trp Tyr Gln Tyr Asp Lys Pro Leu Gly Arg Ile His Lys Pro  
 580                   585                   590  
  
 Asp Pro Trp Leu Ser Thr Phe Leu Ser Arg Tyr Arg Lys Pro His His  
 595                   600                   605  
  
 Ile Glu Pro Arg Thr Ile Ser Gln Asp Glu Ile Leu Glu Arg Cys Leu  
 610                   615                   620  
  
 Tyr Ser Leu Ile Asn Glu Ala Phe Arg Ile Leu Gly Glu Gly Ile Ala  
 625                   630                   635                   640  
  
 Ala Ser Pro Glu His Ile Asp Val Val Tyr Leu His Gly Tyr Gly Cys  
 645                   650                   655  
  
 Ala Arg His Lys Gly Gly Pro Met Phe Tyr Ala Ser Thr Val Gly Leu  
 660                   665                   670  
  
 Pro Thr Val Leu Glu Lys Leu Gln Lys Tyr Tyr Arg Gln Asn Pro Asp  
 675                   680                   685  
  
 Ile Pro Gln Leu Glu Pro Ser Asp Tyr Leu Lys Lys Leu Ala Ser Gln  
 690                   695                   700

Gly Asn Pro Pro Leu Lys Glu Trp Gln Ser Leu Ala Gly Ser Pro Ser  
705 710 715 720

Ser Lys Leu

<210> 13  
<211> 2154  
<212> DNA  
<213> Mus musculus

<400> 13  
atggctgagt atctgaggct gccccactcc ctggctatga tccgcctctg caatccacccg 60  
gtcaatgccca tcagtccaaac tgtaatcaca gaagtaagga atggactcca gaaagcttagt 120  
ttggaccata cggttagcgc catagtgatc tgtggagcaa atgacaacctt ctgtgcaggt 180  
gctgatatcc atggctttaa atctcccact ggccttacat taggaagctt ggttagatgaa 240  
atacagcgat accagaagcc agtgtggcc gccatccaag gcgtggctct tggaggagga 300  
ctagagctgg ctttggctg tcactatcg attgccaatg caaaggctcg ttttggcttc 360  
ccggaaatgtga tgctggaaat ttttccctgtt gcaagaggaa cgcagcttcc acccagggtc 420  
gttggagttc ctgttgctct tgacttaatt acctcaggaa gacatatttc aacagatgaa 480  
gcactcaagc ttggaaattct ggatgttagtt gtaaagtccg acccagttga agaagccatc 540  
aaatttgctc agacggttat aggtaaaaccc atagaacccc gcaggatcct aaacaagcca 600  
gtcccaagct tgcccaacat ggacagtgtt tttgcagaag ccattgccaa ggtacggaaag 660  
cagtaccctg gccgcctggc tccggagact tttgtccgtt cagttccaggc ctccgtgaag 720  
catccatatg aagtggccat caaggaagaa gcaagctgt ttatgtaccc tccgggggtcg 780  
ggcaggcta gagccctgca gtacgccttt tttgtcgtaaa agtctgc当地 taagtggctca 840  
actccctcg gacatcttg gaaaacagca tttgtcgtcc acgttccctc gtttgggttt 900  
cttggcttgg gaacgatggg ccgaggcatc gccatcttcc ttgtcaagggt gggatccct 960  
gtgggtgtcg tagagtccaa cccaaagcag ctagatactg caaagaagat aataacttcc 1020  
accttggaaa aggaagcatc gaagagtggc caagcttcg caaaaacccaa cctcagggttc 1080  
tcctcatcca caaaggagct ttcgagtttgc gatgttgc ttgtcaaggat gttcgtcc 1140  
atgaacctga agaagaaggt cttcgctgaa ctgtcagccc tttgtcaagcc gggagcttt 1200  
ctgtgcacca atacctcgac actggatgtg gatgtaccc tttttccac agatcgcccc 1260  
cagctggta ttggcacccca cttttctcc ccagccacaca tcatgagggtt actagagggtc 1320  
atccctagcc gatactcttc ccccaactacc atcgccacag tcatgaggctt atccaaaagg 1380  
atggaaaaga ttggagtcgt tttttgttac tgctatggat ttgttggaa tttgttgc 1440  
gtcccttattt acaaccagggtt ctatcccttg atagaggaag gtagtaagcc agaggatgt 1500  
gatgggggtct tagaagaggtt tgggtttaga atggggccct tcagggtgtc tttgttgc 1560  
gggcttagatg tgggttggaa agttcgccaa gggcaaggcc ttactggacc gtccttaccc 1620  
ccaggaaccc ccacccgaaa gaggggcaat accaggtact ccccaattgc tttgttgc 1680  
ttgtgaagtcg ggcattttgg tcagaagaca ggttgggtt ggtatcgtt tttgttgc 1740  
ctgggtcgca tccacaaacc ttttttttttgc ctttttttttgc ttttttttttgc 1800  
accatcaca tcaaggcagcg ctccatcagc aaggaggaaa ttttttttttgc ttttttttttgc 1860  
ttcccttatca acgaggcatt ccgcattttgc gaggaggaaa ttttttttttgc ttttttttttgc 1920  
atggatgtca ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 1980  
ttatgttgcctt ctttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 2040

aatccctgaca tcccccagct ggagcccagt gactacctga ggaggctggc tgcccaggga 2100  
 agcccttcctc tgaaaagaatg gcaaagcttg gcaggaccgc atagcagcaa actg 2154

<210> 14  
 <211> 718  
 <212> PRT  
 <213> Mus musculus

<400> 14

Met	Ala	Glu	Tyr	Leu	Arg	Leu	Pro	His	Ser	Leu	Ala	Met	Ile	Arg	Leu
1				5					10			15			

Cys Asn Pro Pro Val Asn Ala Ile Ser Pro Thr Val Ile Thr Glu Val  
 20 25 30

Arg Asn Gly Leu Gln Lys Ala Ser Leu Asp His Thr Val Arg Ala Ile  
 35 40 45

Val Ile Cys Gly Ala Asn Asp Asn Phe Cys Ala Gly Ala Asp Ile His  
 50 55 60

Gly Phe Lys Ser Pro Thr Gly Leu Thr Leu Gly Ser Leu Val Asp Glu  
 65 70 75 80

Ile Gln Arg Tyr Gln Lys Pro Val Val Ala Ala Ile Gln Gly Val Ala  
 85 90 95

Leu Gly Gly Leu Glu Leu Ala Leu Gly Cys His Tyr Arg Ile Ala  
 100 105 110

Asn Ala Lys Ala Arg Val Gly Phe Pro Glu Val Met Leu Gly Ile Leu  
 115 120 125

Pro Gly Ala Arg Gly Thr Gln Leu Leu Pro Arg Val Val Gly Val Pro  
 130 135 140

Val Ala Leu Asp Leu Ile Thr Ser Gly Arg His Ile Ser Thr Asp Glu  
 145 150 155 160

Ala Leu Lys Leu Gly Ile Leu Asp Val Val Lys Ser Asp Pro Val  
 165 170 175

Glu Glu Ala Ile Lys Phe Ala Gln Thr Val Ile Gly Lys Pro Ile Glu  
 180 185 190

Pro Arg Arg Ile Leu Asn Lys Pro Val Pro Ser Leu Pro Asn Met Asp  
 195 200 205

Ser Val Phe Ala Glu Ala Ile Ala Lys Val Arg Lys Gln Tyr Pro Gly  
 210 215 220

Arg Leu Ala Pro Glu Thr Cys Val Arg Ser Val Gln Ala Ser Val Lys  
 225 230 235 240

His Pro Tyr Glu Val Ala Ile Lys Glu Ala Lys Leu Phe Met Tyr  
 245 250 255

Leu Arg Gly Ser Gly Gln Ala Arg Ala Leu Gln Tyr Ala Phe Phe Ala  
 260 265 270

Glu Lys Ser Ala Asn Lys Trp Ser Thr Pro Ser Gly Ala Ser Trp Lys  
275 280 285

Thr Ala Ser Ala Gln Pro Val Ser Ser Val Gly Val Leu Gly Leu Gly  
290 295 300

Thr Met Gly Arg Gly Ile Ala Ile Ser Phe Ala Arg Val Gly Ile Pro  
305 310 315 320

Val Val Ala Val Glu Ser Asp Pro Lys Gln Leu Asp Thr Ala Lys Lys  
325 330 335

Ile Ile Thr Ser Thr Leu Glu Lys Glu Ala Ser Lys Ser Gly Gln Ala  
340 345 350

Ser Ala Lys Pro Asn Leu Arg Phe Ser Ser Ser Thr Lys Glu Leu Ser  
355 360 365

Ser Val Asp Leu Val Ile Glu Ala Val Phe Glu Asp Met Asn Leu Lys  
370 375 380

Lys Lys Val Phe Ala Glu Leu Ser Ala Leu Cys Lys Pro Gly Ala Phe  
385 390 395 400

Leu Cys Thr Asn Thr Ser Ala Leu Asp Val Asp Asp Ile Ala Ser Ser  
405 410 415

Thr Asp Arg Pro Gln Leu Val Ile Gly Thr His Phe Phe Ser Pro Ala  
420 425 430

His Ile Met Arg Leu Leu Glu Val Ile Pro Ser Arg Tyr Ser Ser Pro  
435 440 445

Thr Thr Ile Ala Thr Val Met Ser Leu Ser Lys Arg Ile Gly Lys Ile  
450 455 460

Gly Val Val Val Gly Asn Cys Tyr Gly Phe Val Gly Asn Arg Met Leu  
465 470 475 480

Ala Pro Tyr Tyr Asn Gln Gly Tyr Phe Leu Ile Glu Glu Gly Ser Lys  
485 490 495

Pro Glu Asp Val Asp Gly Val Leu Glu Glu Phe Gly Phe Arg Met Gly  
500 505 510

Pro Phe Arg Val Ser Asp Leu Ala Gly Leu Asp Val Gly Trp Lys Val  
515 520 525

Arg Lys Gly Gln Gly Leu Thr Gly Pro Ser Leu Pro Pro Gly Thr Pro  
530 535 540

Thr Arg Lys Arg Gly Asn Thr Arg Tyr Ser Pro Ile Ala Asp Met Leu  
545 550 555 560

Cys Glu Ala Gly Arg Phe Gly Gln Lys Thr Gly Lys Gly Trp Tyr Gln  
565 570 575

Tyr Asp Lys Pro Leu Gly Arg Ile His Lys Pro Asp Pro Trp Leu Ser  
580 585 590

Glu Phe Leu Ser Gln Tyr Arg Glu Thr His His Ile Lys Gln Arg Ser

595	600	605
Ile Ser Lys Glu Glu Ile Leu Glu Arg Cys Leu Tyr Ser Leu Ile Asn		
610	615	620
Glu Ala Phe Arg Ile Leu Glu Glu Gly Met Ala Ala Ser Pro Glu His		
625	630	635
Ile Asp Val Ile Tyr Leu His Gly Tyr Gly Trp Pro Arg His Val Gly		
645	650	655
Gly Pro Met Tyr Tyr Ala Ala Ser Val Gly Leu, Pro Thr Val Leu Glu		
660	665	670
Lys Leu Gln Lys Tyr Tyr Arg Gln Asn Pro Asp Ile Pro Gln Leu Glu		
675	680	685
Pro Ser Asp Tyr Leu Arg Arg Leu Val Ala Gln Gly Ser Pro Pro Leu		
690	695	700
Lys Glu Trp Gln Ser Leu Ala Gly Pro His Ser Ser Lys Leu		
705	710	715
<210> 15		
<211> 2166		
<212> DNA		
<213> Rattus norvegicus		
<400> 15		
atggctgagt atctgaggct gccccactcc ctggcgatga tccgcctctg caacccgcca	60	
gtcaacgccc tcagtccaaac tgtaatcagg gaagtaagaa atggactcca gaaagctgga	120	
ttagaccaca cggtaaaagc cattgtgatc tgtggcCAA acggAAactt ctgtgcaggT	180	
gctgataatcc atggcttttag tgcttttacc cctggcCTTG cattagGAAG ctggTAGAT	240	
gaaatacaga gataccAGAA gCCGGTGTG gCCGCTATCC aAGGTGTGCG tCTCGGAGGA	300	
ggactggAGC tggcTTGGG ctgtcaCTAT CGGATTGCC ATGCAAAGGC tcgtgtCGGC	360	
ttggcAGAAG tcacACTGGG gattCTTCt ggtGCAAGAG GAACCCAGCT tctccccAGG	420	
gtcgTTGGAG ttccTGTGc tcttgacctA attacCTAG gaaaATATCT ttcAGCAGAT	480	
gaAGCActCA ggCTTGGAAAt tctggatGCA gtcgtGAAGT cAGACCCAGT tGAAGAAGCC	540	
atcaaATTCG ctcAGAAGAT tatAGATAAA cccatAGAAC CCCGcAGGAT cttaACAAG	600	
ccAGTTCCAAt gcttGCCAA catGGACAGT gttttGcAG aAGCCATCGC CAAGGTACGA	660	
aaACAGTACC ctggTGTCTT ggctCCGGAG acgtGTGTCC gctcaatCCA ggcctCTGTG	720	
aAGCAtCCt AcGAAGTAGG catCAAGGAA gaggAAAAGC tGTTTATGTA CCTCCGGGCA	780	
tccggcAGG ctaaAGCCt ACAGTATGCC ttctttGCTG AAAAGTCTGC AAATAAGTGG	840	
tcaactCCt caggAGCGTC ttggAAAACA gcctCTGCTC AACCCGTCtC CTCAGTTGGC	900	
gttcttggct tggGAACGAT gggCCGAGGC atcGCCATTt CTTTGCAG AGTGGGGATC	960	
tctgtggTTG ctgtggAGTC AGACCCAAAG CAGCTAGATG CTGCAAAGAA GATAATCACT	1020	
ttcacCTTGG AGAAGGAAGC AtCCAGAGCG catcAGAACG gccaAGCTC ggcaAAACCA	1080	
AAACTCAGGT tctcCTCATC cacaAAAGGA CTTCAACTG TGGATTGgt ggtGAAGCA	1140	
gtgttGAAAG ACATGAACt GAAGAAAAAG gtctttGCTG AGCTGTcAGC CCTGTGCAAG	1200	
ccaggAGCt ttctgtGcAc CAATACCTG gCGCTGAACG TGGACGACAT tGCTTCTTCC	1260	
acagatGCC CTCAGCTGGT gattGGCACC CACTTCTtC caccAGCCCA tGTCATGAGG	1320	

ttgtctagagg	tcatccctag	ccgataactct	tccccacta	ccatcgccac	ggtttatgagc	1380
ttgtccaaaa	agatcgaaa	gattggagta	gtggttggca	actgctatgg	atttgttggg	1440
aatcgatgt	tggctcccta	ttacaaccag	gggttttct	tgttagagga	aggtagcaag	1500
ccagaggatg	tagacggggt	cttggaaagag	tttgggttta	aatgggacc	cttcagagtg	1560
tcagacctcg	cagggctaga	tgtgggttgg	aaaattcgca	aggggcaagg	ccttactgga	1620
ccatcattgc	caccaggac	ccccgtccga	aagaggggca	acagcaggt	ctccccactt	1680
ggcgatatgc	tctgtgaagc	tggcggtt	ggtcagaaga	caggtaaagg	ctggtatcag	1740
tatgacaagc	cactgggtcg	catccacaaa	cctgatccc	ggcttctac	gttcctgtca	1800
caatatagag	aggttcacca	catcgagcag	cgcaccatca	gcaaggagga	gatcctggag	1860
cgttcttat	attecctcat	caatgaggcg	ttccgcatct	tggaggaggg	gatggctgct	1920
cgcaggagc	acattgatgt	catctacttg	cacgggtacg	ggtggccaag	gcacaaggc	1980
ggcccatgt	tctatgctgc	ctcagtggg	ttgcccacag	ttctagagaa	actgcagaaa	2040
tattacaggc	agaaccctga	catccccag	ctggagccca	gtgactacct	.cagaaggctg	2100
gtagccagg	gaagccctcc	tctgaaggaa	tggcaaagct	tggcagggcc	ccacggcagc	2160
aaactg						2166

<210> 16  
<211> 722  
<212> PRT  
<213> Rattus norvegicus

<400> 16

Met	Ala	Glu	Tyr	Leu	Arg	Leu	Pro	His	Ser	Leu	Ala	Met	Ile	Arg	Leu
1				5					10				15		

Cys	Asn	Pro	Pro	Val	Asn	Ala	Val	Ser	Pro	Thr	Val	Ile	Arg	Glu	Val
				20				25				30			

Arg	Asn	Gly	Leu	Gln	Lys	Ala	Gly	Ser	Asp	His	Thr	Val	Lys	Ala	Ile
				35			40				45				

Val	Ile	Cys	Gly	Ala	Asn	Gly	Asn	Phe	Cys	Ala	Gly	Ala	Asp	Ile	His
				50			55			60					

Gly	Phe	Ser	Ala	Phe	Thr	Pro	Gly	Leu	Ala	Leu	Gly	Ser	Leu	Val	Asp
				65		70		75			80				

Glu	Ile	Gln	Arg	Tyr	Gln	Lys	Pro	Val	Leu	Ala	Ala	Ile	Gln	Gly	Val
				85				90				95			

Ala	Leu	Gly	Gly	Leu	Glu	Leu	Ala	Leu	Gly	Cys	His	Tyr	Arg	Ile
				100			105			110				

Ala	Asn	Ala	Lys	Ala	Arg	Val	Gly	Leu	Pro	Glu	Val	Thr	Leu	Gly	Ile
				115			120				125				

Leu	Pro	Gly	Ala	Arg	Gly	Thr	Gln	Leu	Leu	Pro	Arg	Val	Val	Gly	Val
				130		135			140						

Pro	Val	Ala	Leu	Asp	Leu	Ile	Thr	Ser	Gly	Lys	Tyr	Leu	Ser	Ala	Asp
				145			150			155			160		

Glu	Ala	Leu	Arg	Leu	Gly	Ile	Leu	Asp	Ala	Val	Val	Lys	Ser	Asp	Pro
				165			170				175				

Val Glu Glu Ala Ile Lys Phe Ala Gln Lys Ile Ile Asp Lys Pro Ile  
 180 185 190  
  
 Glu Pro Arg Arg Ile Phe Asn Lys Pro Val Pro Ser Leu Pro Asn Met  
 195 200 205  
  
 Asp Ser Val Phe Ala Glu Ala Ile Ala Lys Val Arg Lys Gln Tyr Pro  
 210 215 220  
  
 Gly Val Leu Ala Pro Glu Thr Cys Val Arg Ser Ile Gln Ala Ser Val  
 225 230 235 240  
  
 Lys His Pro Tyr Glu Val Gly Ile Lys Glu Glu Glu Lys Leu Phe Met  
 245 250 255  
  
 Tyr Leu Arg Ala Ser Gly Gln Ala Lys Ala Leu Gln Tyr Ala Phe Phe  
 260 265 270  
  
 Ala Glu Lys Ser Ala Asn Lys Trp Ser Thr Pro Ser Gly Ala Ser Trp  
 275 280 285  
  
 Lys Thr Ala Ser Ala Gln Pro Val Ser Ser Val Gly Val Leu Gly Leu  
 290 295 300  
  
 Gly Thr Met Gly Arg Gly Ile Ala Ile Ser Phe Ala Arg Val Gly Ile  
 305 310 315 320  
  
 Ser Val Val Ala Val Glu Ser Asp Pro Lys Gln Leu Asp Ala Ala Lys  
 325 330 335  
  
 Lys Ile Ile Thr Phe Thr Leu Glu Lys Glu Ala Ser Arg Ala His Gln  
 340 345 350  
  
 Asn Gly Gln Ala Ser Ala Lys Pro Lys Leu Arg Phe Ser Ser Ser Thr  
 355 360 365  
  
 Lys Glu Leu Ser Thr Val Asp Leu Val Val Glu Ala Val Phe Glu Asp  
 370 375 380  
  
 Met Asn Leu Lys Lys Val Phe Ala Glu Leu Ser Ala Leu Cys Lys  
 385 390 395 400  
  
 Pro Gly Ala Phe Leu Cys Thr Asn Thr Ser Ala Leu Asn Val Asp Asp  
 405 410 415  
  
 Ile Ala Ser Ser Thr Asp Arg Pro Gln Leu Val Ile Gly Thr His Phe  
 420 425 430  
  
 Phe Ser Pro Ala His Val Met Arg Leu Leu Glu Val Ile Pro Ser Arg  
 435 440 445  
  
 Tyr Ser Ser Pro Thr Thr Ile Ala Thr Val Met Ser Leu Ser Lys Lys  
 450 455 460  
  
 Ile Gly Lys Ile Gly Val Val Val Gly Asn Cys Tyr Gly Phe Val Gly  
 465 470 475 480  
  
 Asn Arg Met Leu Ala Pro Tyr Tyr Asn Gln Gly Phe Phe Leu Leu Glu  
 485 490 495

Glu Gly Ser Lys Pro Glu Asp Val Asp Gly Val Leu Glu Glu Phe Gly  
500 505 510

Phe Lys Met Gly Pro Phe Arg Val Ser Asp Leu Ala Gly Leu Asp Val  
515 520 525

Gly Trp Lys Ile Arg Lys Gly Gln Gly Leu Thr Gly Pro Ser Leu Pro  
530 535 540

Pro Gly Thr Pro Val Arg Lys Arg Gly Asn Ser Arg Tyr Ser Pro Leu  
545 550 555 560

Gly Asp Met Leu Cys Glu Ala Gly Arg Phe Gly Gln Lys Thr Gly Lys  
565 570 575

Gly Trp Tyr Gln Tyr Asp Lys Pro Leu Gly Arg Ile His Lys Pro Asp  
580 585 590

Pro Trp Leu Ser Thr Phe Leu Ser Gln Tyr Arg Glu Val His His Ile  
595 600 605

Glu Gln Arg Thr Ile Ser Lys Glu Glu Ile Leu Glu Arg Cys Leu Tyr  
610 615 620

Ser Leu Ile Asn Glu Ala Phe Arg Ile Leu Glu Glu Gly Met Ala Ala  
625 630 635 640

Arg Pro Glu His Ile Asp Val Ile Tyr Leu His Gly Tyr Gly Trp Pro  
645 650 655

Arg His Lys Gly Gly Pro Met Phe Tyr Ala Ala Ser Val Gly Leu Pro  
660 665 670

Thr Val Leu Glu Lys Leu Gln Lys Tyr Tyr Arg Gln Asn Pro Asp Ile  
675 680 685

Pro Gln Leu Glu Pro Ser Asp Tyr Leu Arg Arg Leu Val Ala Gln Gly  
690 695 700

Ser Pro Pro Leu Lys Glu Trp Gln Ser Leu Ala Gly Pro His Gly Ser  
705 710 715 720

Lys Leu